

1 GAATTCGGCGGAGGCCGAGAGAGAAGTCACTTGGCTTACCTTGAAGTGGTTCTCAGGGTTGGGCGAGAGTGGGGTGGGACCGAGATGC
101 AGCTCTATCCTGTGCCCCCTGGTCGACAGGCCAGCGCTTGGCGTGTCTACTTGGCCCTGTCCGCTGCCGCCCTAATGAGCTCAGGTCTAGGCCGAG
201 CAGAGGGGACCTGGTCGACTCGGTGGCTCGGGCGGCCCGCCCTCCCCCGCCCGCAGCGCGGCCCTTCTCGACGGCGGGGGCGGCCCTTGGCG
301 GCGCGGGGCTGAAGGCGGAACCAACGACGCGGCGAGAGACGAGCCGGGAAGCCCTGGGCGCCCGTCGGAGGGCTATGGAGCAGCGGCCCGGGGCTGC
1 M E Q R P R G C
401 GCGGCGGTGGCGGGCGGCTCCTCGTGGTGGTGGGGCCCCAGGGCGGCACTCGTAGCCCCCAGGTGTGACTGTGCCGGTGACTTCCACAAGA
9 A A V A A A L L V L L G A R A Q G G T R S P R C D C A G D F H K K
501 AGATTGGTCTGTTTGTGACAGAGGCTGCCAGCGGGCACTACCTGAAGCCCTTGCACGGAGCCCTGGGCAACTCCACCTGCCCTTGTGTGCCCA
43 I G L F C C R G C P A G H Y L K A P C T E P C G N S T C L V C P Q
601 AGACACCTTCTTGGCCTGGGAGAACCAACATAATTCTGAATGTGCCCGCTGCCAGGCCCTGTGATGAGCAGGCCCTCCAGGTGGCGTGGAGAACTGTTCA
76 D T F L A W E N H H N S E C A R C Q A C D E Q A S Q V A L E N C S
701 GCAGTGGCCGACACCCGCTGTGGCTGTAAAGCCAGGCTGTTGTGGAGTGCCAGGTCAGCCAATGTGTGTCAGCAGTTTACCCCTTCTACTGCCAACCATGCC
109 A V A D T R C G C K P G W F V E C Q V S Q C V S S P F Y C Q P C L
801 TAGACTGCGGGCCCTGCACCGCCACACAGGCTACTCTGTTCGCCGAGAGATACTGACTGTGGGACCTGCCCTGCCCTTCTATGAACATGGCGATGG
143 D C G A L H R H T R L L C S R R D T D C G T C L P G F Y E H G D G
901 CTGCGTGTCTGCCCCACGTAATTCCTAGCTGTCTGGATGGAGGGAAGGGCGCTGGGAGCAGAGCAGGGGCCCTGGGGTGGGCGAGGTGCTGCTGGTT
176 C V S C P T
1001 CAGGAATAGGAAGGGGATAGGAGAGGGAGCCCTTGGCCCTGTGATGGTGGGCCCCACTTCAGGCAAACTTAGATGGCAAAAGAGCAATCTGGATCC
1101 GCCTTAGCCAGATACATAAGGGTATTTGCCCTTCACTTTCAGCCAGCATTCGCCCCAGCGATCCTAGCCAGATATTACAGATGATTTGTCACTTACACAGA
1201 GAGTCACATTGATATAGCTTTAAAACTTGGGCTGAAGGAGGTGAGGCTGCAGTGAGCTATGATCGTGGCCACTGCACCTTCAGCCTGGGCAACAGAGCGAG
1301 ACCTATTAAATAAAATAATTAATAATTAATAATTAATAATCTATTAAATAAATAAATAAAGGGCTGAGAGTCAGGACTGTGCTGC
1401 TAGTTCTCTAGGGGATCTTGGCAAGTGCAGAGAATTC

FIG. 1

	34	D C A G D - - F H K K I G L F C C R G C P A G H Y L K A P C T E P C G N S T C L - - -	hApo2LI
	43	V C P Q G K - - Y I H P Q N N S I C C T K C H K G T Y L Y N D C P G P G Q D T D C R - - -	htNFR1
	39	T C R L R E - - Y Y D Q T A Q M C C S K C S P G Q H A K V F C T K T - S D T V C D - - -	htNFR2
	42	T C R D O E K E - Y Y E P Q H R I C C S R C P P G T Y V S A K C S R I - R D T V C A - - -	htNFRrp
	48	N L E G L - - - H H D G Q F C H K P C P P G E R K A R D C T V N G D E P D C V - - -	hFAS/ApoI
	31	A C P T G - - - L Y T H S G E C C K A C N L G E G V A Q P C G A - - N Q T V C E - - -	hLNGFR
	25	A C R E K - - - Q Y L I N S Q C C S L C Q P G Q K L V S D C T E F - T E T E C L - - -	hCD40
	26	S C P E R - - - H Y W A Q G K L C C Q M C E P G T F L V K D C D Q H R K A A Q C D - - -	hCD27
	28	T C H G N P S H - Y Y D K A V R R C C Y R C P M G L F P T Q Q C P Q R - - P T D C R K - - -	hCD30
	30	H C V G D T - - - Y P S N D R C C H E C R P G N G M V S R C S R S - Q N T V C R - - -	hOX40

	72	83	77	82	84	66	61	64	68	66
hApo2LI	V	E	S	T	P	P	P	P	Q	P
hTNFR1	C	C	E	A	C	C	G	I	C	P
hTNFR2	P	E	D	S	E	L	E	P	E	G
hTNFRtp	Q	S	T	Y	T	D	S	P	P	G
hFAS/Apo1	D	A	E	S	N	E	H	F	S	S
hLINGFR	K	E	Y	T	D	K	A	H	F	S
hCD40	T	F	L	A	W	E	N	H	H	S
hCD27	E	S	G	-	S	F	T	A	S	E
hCD30	S	E	D	S	T	Y	T	Q	L	W
hOX40	P	C	E	G	K	E	Y	T	D	K

FIG. 2A

	116	127	120	126	129	109	105	106	108	109
hApo2LI	C K P G	C R K N	C R P G	C Q P G	C K P N	C A Y G	C E E G	C R N G	- C R P G	- C R A G
hTNFR1	W F V E C Q V S Q C V S S P F Y C	Q Y R H Y W S E N L - - - F Q C	W Y C A L S K Q E G C - - - R L C	M F C A A W A L E C - - - T H C	N F F - - C N S T V C - - - E H C	Y Y Q D E T T - - - - G R C	W H C T S E A C - - - - - E S C	W Q C R D K E C - - - - - T E C	M F C S T S A V N S C - - - A R C	T Q P L D S Y K P G - - - - V D C A
hTNFR2	V E C Q V S Q C V S S P F Y C	R H Y W S E N L - - - F Q C	C A L S K Q E G C - - - R L C	F C A A W A L E C - - - T H C	- - - C N S T V C - - - E H C	Q D E T T - - - - G R C	C T S E A C - - - - - E S C	C R D K E C - - - - - T E C	C S T S A V N S C - - - A R C	P L D S Y K P G - - - - V D C A
hTNFR1p	W F V E C Q V S Q C V S S P F Y C	Q Y R H Y W S E N L - - - F Q C	W Y C A L S K Q E G C - - - R L C	M F C A A W A L E C - - - T H C	N F F - - C N S T V C - - - E H C	Y Y Q D E T T - - - - G R C	W H C T S E A C - - - - - E S C	W Q C R D K E C - - - - - T E C	M F C S T S A V N S C - - - A R C	T Q P L D S Y K P G - - - - V D C A
hFAS/Apo1	W F V E C Q V S Q C V S S P F Y C	Q Y R H Y W S E N L - - - F Q C	W Y C A L S K Q E G C - - - R L C	M F C A A W A L E C - - - T H C	N F F - - C N S T V C - - - E H C	Y Y Q D E T T - - - - G R C	W H C T S E A C - - - - - E S C	W Q C R D K E C - - - - - T E C	M F C S T S A V N S C - - - A R C	T Q P L D S Y K P G - - - - V D C A
hLINGFR	W F V E C Q V S Q C V S S P F Y C	Q Y R H Y W S E N L - - - F Q C	W Y C A L S K Q E G C - - - R L C	M F C A A W A L E C - - - T H C	N F F - - C N S T V C - - - E H C	Y Y Q D E T T - - - - G R C	W H C T S E A C - - - - - E S C	W Q C R D K E C - - - - - T E C	M F C S T S A V N S C - - - A R C	T Q P L D S Y K P G - - - - V D C A
hCD40	W F V E C Q V S Q C V S S P F Y C	Q Y R H Y W S E N L - - - F Q C	W Y C A L S K Q E G C - - - R L C	M F C A A W A L E C - - - T H C	N F F - - C N S T V C - - - E H C	Y Y Q D E T T - - - - G R C	W H C T S E A C - - - - - E S C	W Q C R D K E C - - - - - T E C	M F C S T S A V N S C - - - A R C	T Q P L D S Y K P G - - - - V D C A
hCD27	W F V E C Q V S Q C V S S P F Y C	Q Y R H Y W S E N L - - - F Q C	W Y C A L S K Q E G C - - - R L C	M F C A A W A L E C - - - T H C	N F F - - C N S T V C - - - E H C	Y Y Q D E T T - - - - G R C	W H C T S E A C - - - - - E S C	W Q C R D K E C - - - - - T E C	M F C S T S A V N S C - - - A R C	T Q P L D S Y K P G - - - - V D C A
hCD30	W F V E C Q V S Q C V S S P F Y C	Q Y R H Y W S E N L - - - F Q C	W Y C A L S K Q E G C - - - R L C	M F C A A W A L E C - - - T H C	N F F - - C N S T V C - - - E H C	Y Y Q D E T T - - - - G R C	W H C T S E A C - - - - - E S C	W Q C R D K E C - - - - - T E C	M F C S T S A V N S C - - - A R C	T Q P L D S Y K P G - - - - V D C A
hOX40	W F V E C Q V S Q C V S S P F Y C	Q Y R H Y W S E N L - - - F Q C	W Y C A L S K Q E G C - - - R L C	M F C A A W A L E C - - - T H C	N F F - - C N S T V C - - - E H C	Y Y Q D E T T - - - - G R C	W H C T S E A C - - - - - E S C	W Q C R D K E C - - - - - T E C	M F C S T S A V N S C - - - A R C	T Q P L D S Y K P G - - - - V D C A

[illegible]

FIG. 2B

1 CGGGCCCTGC GGGCGGGGG CTGAAGGCGG AACACGACG GGCAGAGAGC ACGAGCCCGG
61 GAAGCCCCCTG GGCGCCCGTC GGAGGGCTAT GGAGCAGCGG CCGCGGGGCT GCGCGGCGGT
1 M E O R P R G C A A V
121 GGGGGGGCG CTCCTCCTGG TGCTGCTGG GGGCGGGCC CAGGGCGGCA CTCGTAGCCC
12 A A A L L L V L L G A R A Q G G T R S P
181 CAGGTGTGAC TGTGCCGGTG ACTTCCACAA GAAGATTGGT CTGTTTGTG GCAGAGGCTG
32 R C D C A G D F H K K I G L F C C R G C
241 CCCAGCGGG CACTACCTGA AGGCCCTTG CAGGAGCCC TGGGGCAACT CCACCTGCCT
52 P A G H Y L K A P C T E P C G N S T C L
301 TGTGTGTCCC CAAGACACCT TCTTGGCGTG GGAGAACAC CATAATTCTG AATGTGCCCCG
72 V C P Q D T F L A W E N H H N S E C A R
361 CTGCCAGGCC TGTGATGAGC AGGCTCCCA GGTGGCGCTG GAGAACTGTT CAGCAGTGGC
92 C Q A C D E Q A S Q V A L E N C S A V A
421 CGACACCCGC TGTGGCTGTA AGCCAGGCTG GTTGTGGAG TGGCAGGTCA GCCAATGTGT
112 D T R C G C K P G W F V E C Q V S Q C V
481 CAGCAGTTCA CCCTTCTACT GCCAACCATG CCTAGACTGC GGGGCCCTGC ACCGCCACAC
132 S S S P F Y C Q P C L D C G A L H R H T

FIG. 4A

541 ACGGCTACTC TGTTCCCGCA GAGATACTGA CTGTGGGACC TGCCTGCCTG GCTTCTATGA
 152 R L L C S R R D T D C G T C L P G F Y E

 601 ACATGGCGAT GGCTGCGTGT CCTGCCCCAC GAGCACCCCTG GGGAGCTGTC CAGAGCGCTG
 172 H G D G C V S C P T S T L G S C P E R C

 661 TGCCGCTGTC TGTGGCTGGA GGCAGATGTT CTGGGTCCAG GTGCTCCTGG CTGGCCTTGT
 192 A A V C G W R Q M F W V Q V L L A G L V

 721 GGTCCTCCCTC CTGCTTGGGG CCACCCCTGAC CTACACATAC CGCCACTGCT GGCCTCACAA
 212 V P L L L G A T L T Y T Y R H C W P H K

 781 GCCCCCTGGTT ACTGCAGATG AAGCTGGGAT GGAGGCTCTG ACCCCACCAC CGGCCACCCA
 232 P L V T A D E A G M E A L T P P P A T H

 841 TCCTGTCACCC TTGGACAGCG CCCACACCCCT TCTAGCACCT CCTGACAGCA GTGAGAAGAT
 252 L S P L D S A H T L L A P P D S S E K I

 901 CTGCACCGTC CAGTTGGTGG GTAACAGCTG GACCCCTGGC TACCCCGAGA CCCAGGAGGC
 272 C T V Q L V G N S W T P G Y P E T Q E A

 961 GCTCTGCCCG CAGGTGACAT GGTCTCTGGA CCAGTTGCCC AGCAGAGCTC TTGGCCCCCG
 292 L C P Q V T W S W D Q L P S R A L G P A

 1021 TGCTGCGCCC ACACCTCTCG CAGAGTCCCC AGCCGGCTCG CCAGCCATGA TGCTGCAGCC
 312 A A P T L S P E S P A G S P A M M L Q P

FIG. 4B

1081 GGGCCCCGACG CTCTACGACG TGATGGACGC GGTCCCACGC CGGCGCTGGA AGGAGTTCGT
332 G P Q L Y D V M D A V P A R R W K E F V
1141 GCGCACGCTG GGGCTGCGCG AGGCAGAGAT CGAAGCCCGTG GAGGTGGAGA TCGGCCCGCTT
352 R T L G L R E A E I E A V E V E I G R F
1201 CCGAGACCAG CAGTACGAGA TGCTCAAGCG CTGGCGCCAG CAGCAGCCCCG CGGGCCCTCGG
372 R D Q Q Y E M L K R W R Q Q Q P A G L G
1261 AGCCGTTTAC GCGGCCCTGG AGCGCATGGG GCTGGACGGC TGCGTGGAAG ACTTGCGCAG
392 A V Y A A L E R M G L D G C V E D L R S
1321 CCGCCTGCAG CGCGGCCCGGT GACACGGCGC CCACTTGCCA CCTAGGCGCT CTGGTGGCCC
412 R L Q R G P
1381 TTGCAGAAGC CCTAAGTACG GTTACTTATG CGTGTAGACA TTTTATGTCA CTTATTAAAGC
1441 CGCTGGCAGC GCCCTGCGTA GCAGCACCCAG CCGGCCCCAC CCCTGCTCGC CCCTATCGCT
1501 CCAGCCAAGG CGAAGAAGCA CGAACGAATG TCGAGAGGGG GTGAAGACAT TTCTCAACTT
1561 CTCGGCCGGA GTTTGGCTGA GATCGCGGTA TTAAATCTGT GAAAGAAAAC AAAAAAAA
1621 AAAAAAAAAA AAAA

FIG. 4C

Apo3	338	VMDA	VPA	RRWK	EFV	RTL	GL	REA	EIE	EA	VE	VE	IGR	-	-	FR	QQ	YE
TNFR1	333	VVEN	VPL	RWK	EFV	RR	LG	L	SD	HE	IDL	EL	QNG	R	-	CL	RE	AQYS
Fas/Apo1	220	IAGV	MTLS	QVK	G	FV	RKNG	VNE	AK	ID	E	IK	NDN	VQD	TA	E	QKV	-Q
FADD	104	ICDN	VGK	-D	WR	RL	A	RQ	LKV	SD	T	K	ID	S	I	ED	RY	PN
TRADD	211	NRPL	SLK	-D	QT	F	ARS	VG	L	K	WR	KK	VGR	-S	LQ	R	G	CRA
RIP	291	IREN	LGK	-H	KN	CA	R	KL	G	FT	Q	S	A	I	D	E	I	DH
Reaper	1				MA	V	FY	I	P	D	Q	A	T	L	L	R	E	A

Apo3	378	ML	KRW	RQ	Q	P	-	-	-	A	G	L	G	A	V	A	A	L	E	R	M	G	L	-	D	G	C	V	E	D	L	R	S						
TNFR1	374	ML	A	T	W	R	R	R	R	E	A	T	L	E	L	L	G	R	V	L	R	D	M	D	L	-	L	G	C	L	E	D	I	E	E				
Fas/Apo1	261	L	L	R	N	W	H	Q	L	H	G	-	K	K	E	A	Y	D	T	L	I	K	D	L	K	K	A	N	L	C	T	L	A	-	E	K	I	Q	T
FADD	144	S	L	R	I	W	K	N	T	E	-	K	E	N	A	T	V	A	H	L	V	G	A	L	R	S	C	-	-	Q	M	N	L	V	A	D	L	V	
TRADD	251	S	L	A	Y	E	E	R	E	G	L	Y	E	Q	A	F	Q	L	L	R	R	F	V	-	Q	A	E	G	R	R	A	T	L	Q	R	L	V	E	
RIP	332	ML	Q	K	W	V	M	R	E	G	I	K	G	A	T	V	G	K	L	A	Q	A	L	H	Q	C	-	-	S	R	I	D	L	L	S	S	L	T	
Reaper	34	FL	A	T	V	V	L	E	T	L	K	Q	Y	T	S	C	H	P	K	T	G	R	K	S	G	K	Y	R	K	P									

FIG. 6

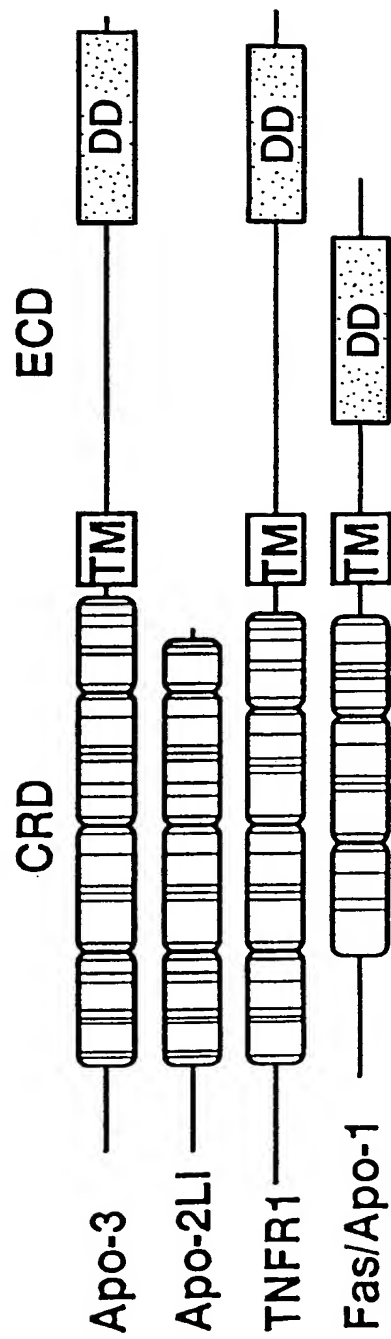


FIG. 7

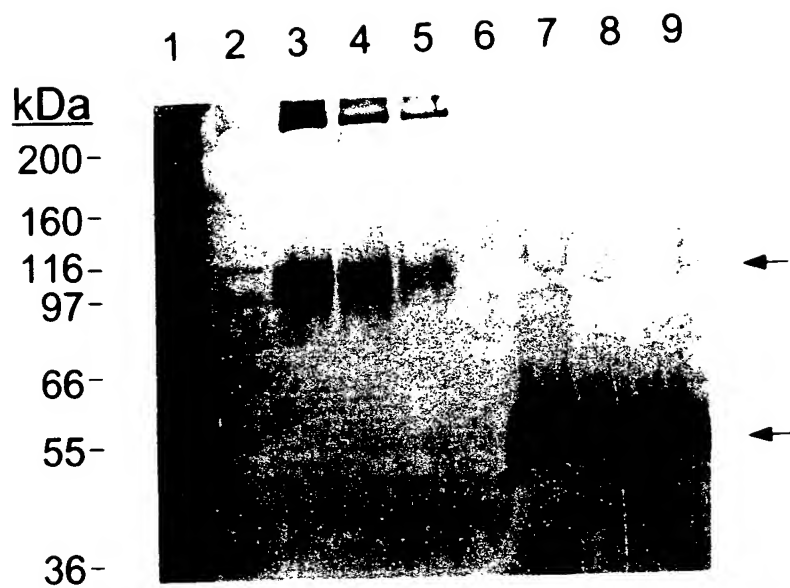


FIG. 3

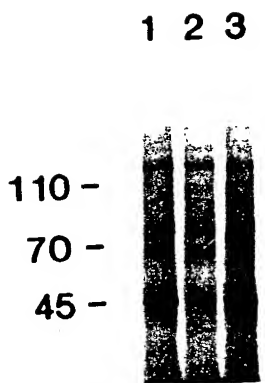


FIG. 8

1 2 3 4 5 6 7 8 9



FIG. 10

FIG. 9A



FIG. 9B



FIG. 9C



FIG. 9D



FIG. 9E

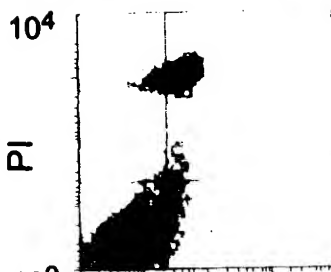


FIG. 9F

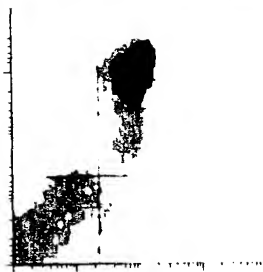


FIG. 9G

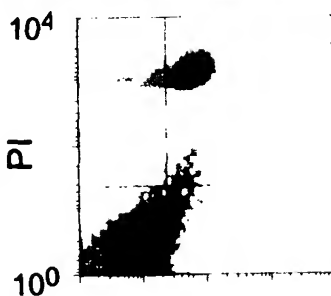


FIG. 9H

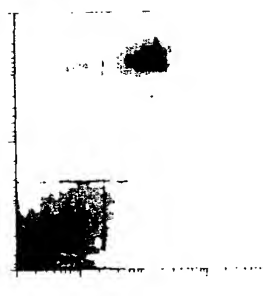


FIG. 9I

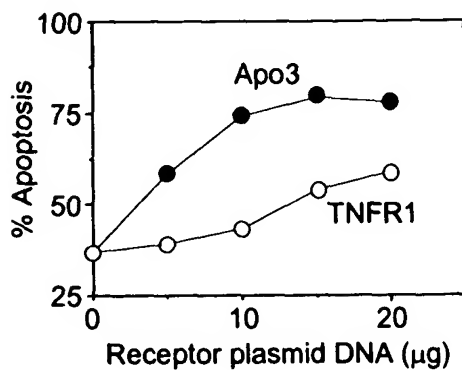


FIG. 9J



Transfection

pRK5
TNFR1
Apo-3

 **Phospho-C-Jun**

FIG. 11

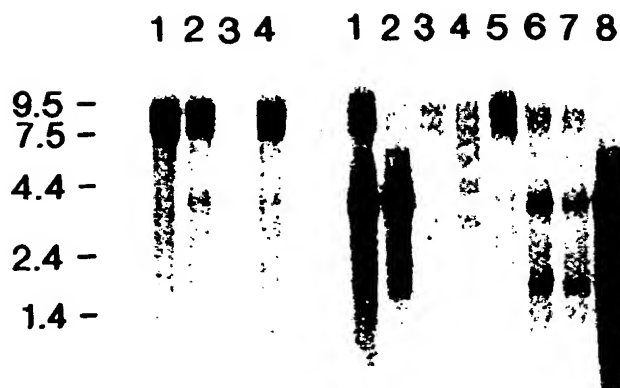


FIG. 12